Package 'data.tree'

November 12, 2023

Version 1.1.0 Date 2023-11-11 VignetteBuilder knitr, rmarkdown Imports R6, stringi, methods Suggests Formula, graphics, testthat, knitr, rmarkdown, ape, yaml, networkD3, jsonlite, treemap, party, partykit, doParallel, foreach, htmlwidgets, DiagrammeR (>= 1.0.0), mockery, rpart Enhances igraph Description Create tree structures from hierarchical data, and traverse the tree in various orders. Aggregate, cumulate, print, plot, convert to and from data.frame and more. Useful for decision trees, machine learning, finance, conversion from and to JSON, and many other applications. **License** GPL (>= 2) URL https://github.com/gluc/data.tree BugReports https://github.com/gluc/data.tree/issues **Depends** R (>= 3.5) RoxygenNote 7.2.3 **Encoding UTF-8** NeedsCompilation no Author Russ Hyde [ctb] (improve dependencies), Chris Hammill [ctb] (improve getting), Facundo Munoz [ctb] (improve list conversion), Markus Wamser [ctb] (fixed some typos), Pierre Formont [ctb] (additional features), Kent Russel [ctb] (documentation), Noam Ross [ctb] (fixes), Duncan Garmonsway [ctb] (fixes),

Christoph Glur [aut, cre] (R interface)

Title General Purpose Hierarchical Data Structure

Type Package

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Repository CRAN

Date/Publication 2023-11-12 20:23:21 UTC

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acme

Sample Data: A Simple Company with Departments

Description

acme's tree representation is accessed through its root, acme.

Usage

data(acme)

Format

A data.tree root Node

Details

- cost, only available for leaf nodes. Cost of the project.
- p probability that a project will be undertaken.

Aggregate

Aggregate child values of a Node, recursively.

Description

The Aggregate method lets you fetch an attribute from a Node's children, and then aggregate them using aggFun. For example, you can aggregate cost by summing costs of child Nodes. This is especially useful in the context of tree traversal, when using post-order traversal mode.

Usage

```
Aggregate(node, attribute, aggFun, ...)
```

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Arguments

Details

As with Get, the attribute can be a field, a method or a function. If the attribute on a child is NULL, Aggregate is called recursively on its children.

See Also

Node

```
data(acme)
#Aggregate on a field
Aggregate(acme, "cost", sum)
#This is the same as:
HomeRolledAggregate <- function(node) {</pre>
 sum(sapply(node$children, function(child) {
    if (!is.null(child$cost)) child$cost
    else HomeRolledAggregate(child)
 }))
HomeRolledAggregate(acme)
#Aggregate using Get
print(acme, "cost", minCost = acme$Get(Aggregate, "cost", min))
#use Aggregate with a function:
Aggregate(acme, function(x) x$cost * x$p, sum)
#cache values along the way
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum), traversal = "post-order")</pre>
acme$IT$cost
```

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AreNamesUnique

Test whether all node names are unique.

Description

This can be useful for some conversions.

Usage

AreNamesUnique(node)

Arguments

node

The root Node of the data. tree structure to test

Value

TRUE if all Node\$name == TRUE for all nodes in the tree

See Also

as.igraph.Node

Examples

data(acme)
AreNamesUnique(acme)
acme\$name <- "IT"
AreNamesUnique(acme)</pre>

as.data.frame.Node

Convert a data. tree structure to a data. frame

Description

If a node field contains data of length > 1, then that is converted into a string in the data.frame.

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Usage

```
## S3 method for class 'Node'
as.data.frame(
 Х,
 row.names = NULL,
 optional = FALSE,
  traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
 pruneFun = NULL,
 filterFun = NULL,
 format = FALSE,
 inheritFromAncestors = FALSE
)
ToDataFrameTree(x, ..., pruneFun = NULL)
ToDataFrameTable(x, ..., pruneFun = NULL)
ToDataFrameNetwork(
 Х,
 direction = c("climb", "descend"),
 pruneFun = NULL,
 format = FALSE,
 inheritFromAncestors = FALSE
)
ToDataFrameTypeCol(x, ..., type = "level", prefix = type, pruneFun = NULL)
```

Arguments

x	The root Node of the tree or sub-tree to be convert to a data.frame
row.names	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional	logical. If TRUE, setting row names and converting column names (to syntactic names: see make.names) is optional.
• • •	the attributes to be added as columns of the data.frame. See Get for details. If a specific Node does not contain the attribute, NA is added to the data.frame.
traversal	any of 'pre-order' (the default), 'post-order', 'in-order', 'level', or 'ancestor'. See Traverse for details.
pruneFun	allows providing a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
filterFun	a function taking a Node as an argument. See Traverse for details.
format	if FALSE (the default), then no formatting will be applied. If TRUE, then the first formatter (if any) along the ancestor path is used for formatting.

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inheritFromAncestors

if FALSE, and if the attribute is a field or a method, then only a Node itself is searched for the field/method. If TRUE, and if the Node does not contain the

attribute, then ancestors are also searched.

direction when converting to a network, should the edges point from root to children

("climb") or from child to parent ("descend")?

type when converting type columns, the type is the discriminator, i.e. an attribute

(e.g. field name) of each node

prefix when converting type columns, the prefix used for the column names. Can be

NULL to omit prefixes.

Value

ToDataFrameTree: a data.frame, where each row represents a Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun.

ToDataFrameTable: a data.frame, where each row represents a leaf Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun.

ToDataFrameNetwork: a data.frame, where each row represents a Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun. The first column is called 'from', while the second is called 'to', describing the parent to child edge (for direction "climb") or the child to parent edge (for direction "descend"). If AreNamesUnique is TRUE, then the Network is based on the Node\$name, otherwise on the Node\$pathString

ToDataFrameTypeCol: a data.frame in table format (i.e. where each row represents a leaf in the tree or sub-tree spanned by x), possibly pruned according to pruneFun. In addition to ..., each distinct type is output to a column.

```
data(acme)
acme$attributesAll
as.data.frame(acme, row.names = NULL, optional = FALSE, "cost", "p")
ToDataFrameTree(acme, "cost", "p")
ToDataFrameNetwork(acme, "cost", "p", direction = "climb")
ToDataFrameTable(acme, "cost", "p")
ToDataFrameTypeCol(acme)
#use the pruneFun:
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")
ToDataFrameTree(acme, "totalCost", pruneFun = function(x) x$totalCost > 300000)
#inherit
acme\$Set(floor = c(1, 2, 3), filterFun = function(x) x\$level == 2)
as.data.frame(acme, row.names = NULL, optional = FALSE, "floor", inheritFromAncestors = FALSE)
as.data.frame(acme, row.names = NULL, optional = FALSE, "floor", inheritFromAncestors = TRUE)
#using a function as an attribute:
acme$Accounting$Head <- "Mrs. Numright"</pre>
acme$Research$Head <- "Mr. Stein"
```

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```
acme$IT$Head <- "Mr. Squarehead"
ToDataFrameTable(acme, department = function(x) x$parent$name, "name", "Head", "cost")
#complex TypeCol
acme$IT$Outsource$AddChild("India")
acme$IT$Outsource$AddChild("Poland")
acme$Set(type = c('company', 'department', 'project', 'department', 'project', 'Doject', 'project', 'pro
```

as.dendrogram.Node

Convert a Node to a dendrogram

Description

Convert a data. tree structure to a dendrogram

Usage

```
## S3 method for class 'Node'
as.dendrogram(
  object,
  heightAttribute = DefaultPlotHeight,
  edgetext = FALSE,
   ...
)
```

Arguments

object The Node to convert

heightAttribute

The attribute (field name or function) storing the height

edgetext If TRUE, then the for non-leaf nodes the node name is stored as the dendro-

gram's edge text.

... Additional parameters

Value

An object of class dendrogram

See Also

Other Conversions from Node: ToNewick()

as.igraph.Node

Examples

```
data(acme)
acmed <- as.dendrogram(acme)
plot(acmed, center = TRUE)

#you can take an attribute for the height:
acme$Do( function(x) x$myPlotHeight <- (10 - x$level))
acmed <- as.dendrogram(acme, heightAttribute = "myPlotHeight")
plot(acmed, center = TRUE)

#or directly a function
acmed <- as.dendrogram(acme, heightAttribute = function(x) 10 - x$level)
plot(acmed)</pre>
```

as.igraph.Node

Convert a data. tree structure to an igraph network

Description

This requires the igraph package to be installed. Also, this requires the names of the Nodes to be unique within the data. tree structure.

Usage

```
as.igraph.Node(
    x,
    vertexAttributes = character(),
    edgeAttributes = character(),
    directed = FALSE,
    direction = c("climb", "descend"),
    ...
)
```

Arguments

x The root Node to convert

vertexAttributes

A vector of strings, representing the attributes in the data. tree structure to add

as attributes to the vertices of the igraph

edgeAttributes A vector of strings, representing the attributes in the data. tree structure to add

as edge attributes of the igraph

directed Logical scalar, whether or not to create a directed graph.

direction when converting to a network, should the edges point from root to children

("climb") or from child to parent ("descend")?

... Currently unused.

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Value

```
an igraph object
```

See Also

AreNamesUnique

Examples

```
data(acme)
library(igraph)
ig <- as.igraph(acme, "p", c("level", "isLeaf"))
plot(ig)</pre>
```

as.list.Node

Convert a data. tree structure to a list-of-list structure

Description

Convert a data. tree structure to a list-of-list structure

Usage

```
## S3 method for class 'Node'
as.list(
  х,
  mode = c("simple", "explicit"),
  unname = FALSE,
  nameName = ifelse(unname, "name", ""),
  childrenName = "children",
  rootName = "",
  keepOnly = NULL,
  pruneFun = NULL,
)
ToListSimple(x, nameName = "name", pruneFun = NULL, ...)
ToListExplicit(
  Х,
  unname = FALSE,
  nameName = ifelse(unname, "name", ""),
  childrenName = "children",
  pruneFun = NULL,
)
```

as.Node

Arguments

x The Node to convert

mode How the list is structured. "simple" (the default) will add children directly as

nested lists. "explicit" puts children in a separate nested list called childrenName

unname If TRUE, and if mode is "explicit", then the nested children list will not have

named arguments. This can be useful e.g. in the context of conversion to JSON,

if you prefer the children to be an array rather than named objects.

nameName The name that should be given to the name element

rootName The name of the node. If provided, this overrides Node\$name

keepOnly A character vector of attributes to include in the result. If NULL (the default), all

attributes are kept.

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and

returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the

Node and its entire sub-tree will not be considered.

... Additional parameters passed to as.list.Node

Examples

```
data(acme)
str(ToListSimple(acme))
str(ToListSimple(acme, keepOnly = "cost"))
str(ToListExplicit(acme))
str(ToListExplicit(acme, unname = TRUE))
str(ToListExplicit(acme, unname = TRUE, nameName = "id", childrenName = "descendants"))
```

as.Node

Convert an object to a data. tree data structure

Description

Convert an object to a data. tree data structure

Usage

```
as.Node(x, ...)
```

Arguments

x The object to be converted

. . . Additional arguments

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See Also

```
Other as.Node: as.Node.data.frame(), as.Node.dendrogram(), as.Node.list(), as.Node.phylo(), as.Node.rpart()
```

as.Node.BinaryTree Convert a a SplitNo

 ${\it Convert}~a~a~{\it SplitNode}~{\it from~the~party~package~to~a}~{\it data.tree~structure.}$

Description

Convert a a SplitNode from the party package to a data. tree structure.

Usage

```
## S3 method for class 'BinaryTree'
as.Node(x, ...)
```

Arguments

x The BinaryTree

. . . additional arguments (unused)

as.Node.data.frame

as.Node.data.frame

Convert a data. frame to a data. tree structure

Description

Convert a data. frame to a data. tree structure

Usage

```
## S3 method for class 'data.frame'
as.Node(
 х,
 mode = c("table", "network"),
 pathName = "pathString",
 pathDelimiter = "/",
 colLevels = NULL,
 na.rm = TRUE
)
FromDataFrameTable(
  table,
 pathName = "pathString",
 pathDelimiter = "/",
 colLevels = NULL,
 na.rm = TRUE,
 check = c("check", "no-warn", "no-check")
)
FromDataFrameNetwork(network, check = c("check", "no-warn", "no-check"))
```

Arguments

x	The data.frame in the required format.			
	Any other argument implementations of this might need			
mode	Either "table" (if x is a data.frame in tree or table format) or "network"			
pathName	The name of the column in x containing the path of the row			
pathDelimiter	The delimiter used to separate nodes in pathName			
colLevels	Nested list of column names, determining on what node levels the attributes are written to.			
na.rm	If TRUE, then NA's are treated as NULL and values will not be set on nodes			
table	a data. frame in table or tree format, i.e. having a row for each leaf (and optionally for additional nodes). There should be a column called pathName, separated by pathDelimiter, describing the path of each row.			
check	Either			

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• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)

- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors

network

A data.frame in network format, i.e. it must adhere to the following requirements:

- It must contain as many rows as there are nodes (excluding the root, there is no row for the root)
- Its first and second columns contain the network relationships. This can be either climbing (from parent to children) or descending (from child to parent)
- Its subsequent columns contain the attributes to be set on the nodes
- It must contain a single root
- There are no cycles in the network

Value

The root Node of the data. tree structure

See Also

```
as.data.frame.Node
Other as.Node: as.Node.dendrogram(), as.Node.list(), as.Node.phylo(), as.Node.rpart(), as.Node()
```

```
data(acme)
#Tree
x <- ToDataFrameTree(acme, "pathString", "p", "cost")
x
xN <- as.Node(x)
print(xN, "p", "cost")

#Table
x <- ToDataFrameTable(acme, "pathString", "p", "cost")
x
xN <- FromDataFrameTable(x)
print(xN, "p", "cost")

#More complex Table structure, using colLevels
acme$Set(floor = c(1, 2, 3), filterFun = function(x) x$level == 2)
x <- ToDataFrameTable(acme, "pathString", "floor", "p", "cost")
x</pre>
```

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```
xN <- FromDataFrameTable(x, colLevels = list(NULL, "floor", c("p", "cost")), na.rm = TRUE)
print(xN, "floor", "p", "cost")

#Network
x <- ToDataFrameNetwork(acme, "p", "cost", direction = "climb")
x
xN <- FromDataFrameNetwork(x)
print(xN, "p", "cost")</pre>
```

as.Node.dendrogram

Convert a dendrogram to a data.tree Node

Description

Convert a dendrogram to a data.tree Node

Usage

```
## S3 method for class 'dendrogram'
as.Node(
    x,
    name = "Root",
    heightName = "plotHeight",
    check = c("check", "no-warn", "no-check"),
    ...
)
```

Arguments

x The dendrogram

name The name of the root Node

heightName The name under which the dendrogram's height is stored

check Either

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors

.. Additional parameters

Value

The root Node of a data.tree

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See Also

```
Other as.Node: as.Node.data.frame(), as.Node.list(), as.Node.phylo(), as.Node.rpart(), as.Node()
```

Examples

```
hc <- hclust(dist(USArrests), "ave")
dend1 <- as.dendrogram(hc)
tree1 <- as.Node(dend1)
tree1$attributesAll
tree1$totalCount
tree1$leafCount
tree1$height</pre>
```

as.Node.list

Convert a nested list structure to a data. tree structure

Description

Convert a nested list structure to a data. tree structure

Usage

```
## S3 method for class 'list'
as.Node(
  х,
 mode = c("simple", "explicit"),
 nameName = "name",
  childrenName = "children",
  nodeName = NULL,
  interpretNullAsList = FALSE,
  check = c("check", "no-warn", "no-check"),
)
FromListExplicit(
  explicitList,
  nameName = "name",
  childrenName = "children",
  nodeName = NULL,
  check = c("check", "no-warn", "no-check")
)
FromListSimple(
  simpleList,
  nameName = "name",
```

as.Node.list

```
nodeName = NULL,
interpretNullAsList = FALSE,
check = c("check", "no-warn", "no-check")
)
```

Arguments

x The list to be converted.

mode How the list is structured. "simple" (the default) will interpret any list to be a

child. "explicit" assumes that children are in a nested list called childrenName

nameName The name of the element in the list that should be used as the name, can be

NULL if mode = explicit and the children lists are named, or if an automatic

name (running number) should be assigned

childrenName The name of the element that contains the child list (applies to mode 'explicit'

only).

nodeName A name suggestion for x, if the name cannot be deferred otherwise. This is for

example the case for the root with mode explicit and named lists.

interpretNullAsList

If TRUE, then NULL-valued lists are interpreted as child nodes. Else, they are interpreted as attributes. This has only an effect if mode is "simple".

check Either

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors

.. Any other argument to be passed to generic sub implementations

explicitList A list in which children are in a separate nested list called childrenName.

simpleList A list in which children are stored as nested list alongside other attributes. Any list is interpreted as a child Node

See Also

```
Other as.Node: as.Node.data.frame(), as.Node.dendrogram(), as.Node.phylo(), as.Node.rpart(), as.Node()
```

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```
list(name = "Joseph II",
                                          spouse = "Kathryn",
                                          born = "1839-03-28",
                                          died = "1865-12-19"),
                                     list(name = "Helen",
                                          born = "1840-17-08",
                                          died = "1845-01-01")
                                     )
FromListExplicit(kingJosephs)
kingJosephs <- list(head = "Joseph I",</pre>
                    spouse = "Mary",
                    born = "1818-02-23"
                    died = "1839-08-29",
                    list(head = "Joseph II",
                          spouse = "Kathryn",
                         born = "1839-03-28",
                         died = "1865-12-19"),
                    list(head = "Helen",
                         born = "1840-17-08",
                          died = "1845-01-01")
                   )
FromListSimple(kingJosephs, nameName = "head")
kingJosephs <- list(spouse = "Mary",</pre>
                    born = "1818-02-23",
                    died = "1839-08-29",
                    `Joseph II` = list(spouse = "Kathryn",
                                        born = "1839-03-28",
                                        died = "1865-12-19"),
                    Helen = list(born = "1840-17-08",
                                  died = "1845-01-01")
FromListSimple(kingJosephs, nodeName = "Joseph I")
```

as.Node.party

Convert a a party from the partykit package to a data. tree structure.

Description

Convert a a party from the partykit package to a data. tree structure.

Usage

```
## S3 method for class 'party'
as.Node(x, ...)
```

as.Node.party

Arguments

```
x The party object... other arguments (unused)
```

```
library(partykit)
data("WeatherPlay", package = "partykit")
### splits ###
# split in overcast, humidity, and windy
sp_o <- partysplit(1L, index = 1:3)</pre>
sp_h <- partysplit(3L, breaks = 75)</pre>
sp_w <- partysplit(4L, index = 1:2)</pre>
## query labels
character_split(sp_o)
### nodes ###
## set up partynode structure
pn <- partynode(1L, split = sp_o, kids = list(</pre>
 partynode(2L, split = sp_h, kids = list(
      partynode(3L, info = "yes"),
      partynode(4L, info = "no"))),
 partynode(5L, info = "yes"),
 partynode(6L, split = sp_w, kids = list(
      partynode(7L, info = "yes"),
      partynode(8L, info = "no")))))
### tree ###
## party: associate recursive partynode structure with data
py <- party(pn, WeatherPlay)</pre>
tree <- as.Node(py)</pre>
print(tree,
      "splitname",
      count = function(node) nrow(node$data),
      "splitLevel")
SetNodeStyle(tree,
             label = function(node) paste0(node$name, ": ", node$splitname),
             tooltip = function(node) paste0(nrow(node$data), " observations"),
             fontname = "helvetica")
SetEdgeStyle(tree,
             arrowhead = "none",
             label = function(node) node$splitLevel,
             fontname = "helvetica",
             penwidth = function(node) 12 * nrow(node$data)/nrow(node$root$data),
             color = function(node) {
               paste0("grey",
                      100 - as.integer( 100 * nrow(node$data)/nrow(node$root$data))
             }
```

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as.Node.phylo

Convert a phylo object from the ape package to a Node

Description

Convert a phylo object from the ape package to a Node

Usage

```
## $3 method for class 'phylo'
as.Node(
    X,
    heightName = "plotHeight",
    replaceUnderscores = TRUE,
    namesNotUnique = FALSE,
    ...
)
```

Arguments

x The phylo object to be converted

heightName If the phylo contains edge lengths, then they will be converted to a height and stored in a field named according to this parameter (the default is "height")

replaceUnderscores

if TRUE (the default), then underscores in names are replaced with spaces

namesNotUnique if TRUE, then the name of the Nodes will be prefixed with a unique id. This is useful if the children of a parent have non-unique names.

... any other parameter to be passed to sub-implementations

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See Also

```
Other ape phylo conversions: GetPhyloNr(), as.phylo.Node()
Other as.Node: as.Node.data.frame(), as.Node.dendrogram(), as.Node.list(), as.Node.rpart(), as.Node()
```

Examples

```
#which bird familes have the max height?
library(ape)
data(bird.families)
bf <- as.Node(bird.families)
height <- bf$height
t <- Traverse(bf, filterFun = function(x) x$level == 25)
Get(t, "name")</pre>
```

as.Node.rpart

Convert an rpart object to a data. tree structure

Description

Convert an rpart object to a data. tree structure

Usage

```
## S3 method for class 'rpart'
as.Node(x, digits = getOption("digits") - 3, use.n = FALSE, ...)
```

Arguments

х	the rpart object to be converted
digits	the number of digits to be used for numeric values in labels
use.n	logical. Add cases to labels, see text.rpart for further information
	any other argument to be passed to generic sub implementations

Value

a data.tree object. The tree contains a field rpart.id which references back to the original node id in the row names of the rpart object.

See Also

```
Other as.Node: as.Node.data.frame(), as.Node.dendrogram(), as.Node.list(), as.Node.phylo(), as.Node()
```

22 as.phylo.Node

Examples

```
if (require(rpart)) {
   fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
   as.Node(fit)
}</pre>
```

as.phylo.Node

Convert a Node to a phylo object from the ape package.

Description

This method requires the ape package to be installed and loaded.

Usage

```
as.phylo.Node(x, heightAttribute = DefaultPlotHeight, ...)
```

Arguments

```
x The root Node of the tree or sub-tree to be converted heightAttribute
The attribute (field name or function) storing the height
... any other argument
```

See Also

```
Other ape phylo conversions: GetPhyloNr(), as.Node.phylo()
```

```
library(ape)
data(acme)
acmephylo <- as.phylo(acme)
#plot(acmephylo)</pre>
```

averageBranchingFactor

Calculate the average number of branches each non-leaf has

Description

Calculate the average number of branches each non-leaf has

Usage

```
averageBranchingFactor(node)
```

Arguments

node

The node to calculate the average branching factor for

CheckNameReservedWord Checks whether name is a reserved word, as defined in NODE_RESERVED_NAMES_CONST.

Description

Checks whether name is a reserved word, as defined in NODE_RESERVED_NAMES_CONST.

Usage

```
CheckNameReservedWord(name, check = c("check", "no-warn", "no-check"))
```

Arguments

name

the name to check

check

Either

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors

24 Climb

Climb

Climb a tree from parent to children, by provided criteria.

Description

This method lets you climb the tree, from crutch to crutch. On each Node, the Climb finds the first child having attribute value equal to the the provided argument.

Usage

```
#node$Climb(...)
Climb(node, ...)
```

Arguments

node The root Node of the tree or subtree to climb

an attribute-value pairlist to be searched. For brevity, you can also provide a character vector to search for names.

Value

the Node having path . . . , or NULL if such a path does not exist

See Also

Node

Navigate

```
data(acme)

#the following are all equivalent
Climb(acme, 'IT', 'Outsource')
Climb(acme, name = 'IT', name = 'Outsource')
Climb(acme, 'IT')$Climb('Outsource')
Navigate(acme, path = "IT/Outsource")

Climb(acme, name = 'IT')

Climb(acme, position = c(2, 1))
#or, equivalent:
Climb(acme, position = 2, position = 1)
Climb(acme, name = "IT", cost = 250000)

tree <- CreateRegularTree(5, 2)
tree$Climb(c("1", "1"), position = c(2, 2))$path</pre>
```

Clone 25

Clone	Clone a tree (creates a deep copy)

Description

The method also clones object attributes (such as the formatters), if desired. If the method is called on a non-root, then the parent relationship is not cloned, and the resulting Node will be a root.

Usage

```
Clone(node, pruneFun = NULL, attributes = FALSE)
```

Arguments

node the root node of the tree or sub-tree to clone

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and

returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the

Node and its entire sub-tree will not be considered.

attributes if FALSE, then R class attributes (e.g. formatters and grViz styles) are not

cloned. This makes the method faster.

Value

the clone of the tree or sub-tree

See Also

SetFormat

```
data(acme)
acmeClone <- Clone(acme)
acmeClone$name <- "New Acme"
# acmeClone does not point to the same reference object anymore:
acme$name

#cloning a subtree
data(acme)
itClone <- Clone(acme$IT)
itClone$isRoot</pre>
```

26 CreateRegularTree

CreateRandomTree

Create a tree for demo and testing

Description

Create a tree for demo and testing

Usage

```
CreateRandomTree(nodes = 100, root = Node$new("1"), id = 1)
```

Arguments

nodes The number of nodes to create

root the previous node (for recursion, typically use default value)

id The id (for recursion)

CreateRegularTree

Create a tree for demo and testing

Description

Create a tree for demo and testing

Usage

```
CreateRegularTree(height = 5, branchingFactor = 3, parent = Node$new("1"))
```

Arguments

height the number of levels

branchingFactor

the number of children per node

parent the parent node (for recursion)

Cumulate 27

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Cumulate values among siblings

Description

For example, you can sum up values of siblings before this Node.

Usage

```
Cumulate(node, attribute, aggFun, ...)
```

Arguments

node The node on which we want to cumulate
attribute determines what is collected. The attribute can be

- a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme\$Get("p") or acme\$Get("position")
- b.) the name of a **method** of each Node in the tree, e.g. acme\$Get("levelZeroBased"), where e.g. acme\$levelZeroBased <- function() acme\$level 1
- c.) a **function**, whose first argument must be a Node e.g. acme\$Get(function(node) node\$cost * node\$p)

aggFun the aggregation function to be applied to the children's attributes
... any arguments to be passed on to attribute (in case it's a function)

Examples

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum), traversal = "post-order")
acme$Do(function(x) x$cumCost <- Cumulate(x, "cost", sum))
print(acme, "cost", "cumCost")</pre>
```

DefaultPlotHeight

Calculates the height of a Node given the height of the root.

Description

This function puts leafs at the bottom (not hanging), and makes edges equally long. Useful for easy plotting with third-party packages, e.g. if you have no specific height attribute, e.g. with as.dendrogram.Node, ToNewick, and as.phylo.Node

Usage

```
DefaultPlotHeight(node, rootHeight = 100)
```

28 Do

Arguments

node The node

rootHeight The height of the root

Examples

```
data(acme)
dacme <- as.dendrogram(acme, heightAttribute = function(x) DefaultPlotHeight(x, 200))
plot(dacme, center = TRUE)</pre>
```

Distance

Find the distance between two nodes of the same tree

Description

The distance is measured as the number of edges that need to be traversed to reach node2 when starting from node1.

Usage

```
Distance(node1, node2)
```

Arguments

node1 the first node in the tree

node2 the second node in the same tree

Examples

```
data(acme)
Distance(FindNode(acme, "Outsource"), FindNode(acme, "Research"))
```

Do

Executes a function on a set of nodes

Description

Executes a function on a set of nodes

FindNode 29

Usage

Arguments

nodes The nodes on which to perform the Get (typically obtained via Traverse)

fun the function to execute. The function is expected to be either a Method, or to take a Node as its first argument

any additional parameters to be passed on to fun

See Also

Node Get Set

Traverse

Examples

```
data(acme)
traversal <- Traverse(acme)
Do(traversal, function(node) node$expectedCost <- node$p * node$cost)
print(acme, "expectedCost")</pre>
```

FindNode

Find a node by name in the (sub-)tree

Description

Scans the entire sub-tree spanned by node and returns the first Node having the name specified. This is mainly useful for trees whose name is unique. If AreNamesUnique is FALSE, i.e. if there is more than one Node called name in the tree, then it is undefined which one will be returned. Also note that this method is not particularly fast. See examples for a faster way to index large trees, if you need to do multiple searches. See Traverse if you need to find multiple Nodes.

Usage

```
FindNode(node, name)
```

30 FormatFixedDecimal

Arguments

node The root Node of the tree or sub-tree to search

name The name of the Node to be returned

Value

The first Node whose name matches, or NULL if no such Node is found.

See Also

AreNamesUnique, Traverse

Examples

```
data(acme)
FindNode(acme, "Outsource")

#re-usable hashed index for multiple searches:
if(!AreNamesUnique(acme)) stop("Hashed index works for unique names only!")
trav <- Traverse(acme, "level")
names(trav) <- Get(trav, "name")
nameIndex <- as.environment(trav)
#you could also use hash from package hash instead!
#nameIndex <- hash(trav)
nameIndex$Outsource
nameIndex$IT</pre>
```

FormatFixedDecimal

Format a Number as a Decimal

Description

Simple function that can be used as a format function when converting trees to a data. frame

Usage

```
FormatFixedDecimal(x, digits = 3)
```

Arguments

x a numeric scalar or vector

digits the number of digits to print after the decimal point

Value

A string corresponding to x, suitable for printing

FormatPercent 31

Examples

```
data(acme)
print(acme, prob = acme$Get("p", format = function(x) FormatFixedDecimal(x, 4)))
```

FormatPercent

Format a Number as a Percentage

Description

This utility method can be used as a format function when converting trees to a data. frame

Usage

```
FormatPercent(x, digits = 2, format = "f", ...)
```

Arguments

x A number
 digits The number of digits to print
 format The format to use
 ... Any other argument passed to formatC

Value

A string corresponding to x, suitable for printing

See Also

formatC

```
data(acme)
print(acme, prob = acme$Get("p", format = FormatPercent))
```

32 Get

Get

Traverse a Tree and Collect Values

Description

The Get method is one of the most important ones of the data.tree package. It lets you traverse a tree and collect values along the way. Alternatively, you can call a method or a function on each Node.

Usage

```
# 00-style:
#node$Get(attribute,
      traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
#
#
         pruneFun = NULL,
         filterFun = NULL,
         format = FALSE,
         inheritFromAncestors = FALSE)
# traditional:
Get(nodes,
    attribute,
    . . . ,
    format = FALSE,
    inheritFromAncestors = FALSE,
    simplify = c(TRUE, FALSE, "array", "regular"))
```

Arguments

nodes

The nodes on which to perform the Get (typically obtained via Traverse)

attribute

determines what is collected. The attribute can be

- a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme\$Get("p") or acme\$Get("position")
- b.) the name of a **method** of each Node in the tree, e.g. acme\$Get("levelZeroBased"), where e.g. acme\$levelZeroBased <- function() acme\$level 1
- c.) a **function**, whose first argument must be a Node e.g. acme\$Get(function(node) node\$cost * node\$p)

. . .

in case the attribute is a function or a method, the ellipsis is passed to it as additional arguments.

format

if FALSE (the default), no formatting is being used. If TRUE, then the first formatter (if any) found along the ancestor path is being used for formatting (see SetFormat). If format is a function, then the collected value is passed to that function, and the result is returned.

GetAttribute 33

inheritFromAncestors

if TRUE, then the path above a Node is searched to get the ${\tt attribute}$ in case it

is NULL.

simplify

same as sapply, i.e. TRUE, FALSE or "array". Additionally, you can specify "regular" if each returned value is of length > 1, and equally named. See below

for an example.

Value

a vector containing the atrributes collected during traversal, in traversal order. NULL is converted to NA, such that length(Node\$Get) == Node\$totalCount

See Also

Node

Set

Do

Traverse

Examples

GetAttribute

Get an attribute from a Node.

Description

Get an attribute from a Node.

34 GetPhyloNr

Usage

```
GetAttribute(
  node,
  attribute,
  ...,
  format = FALSE,
  inheritFromAncestors = FALSE,
  nullAsNa = TRUE
)
```

Arguments

node The Node from which the attribute should be fetched.

attribute determines what is collected. The attribute can be

- a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme\$Get("p") or acme\$Get("position")
- b.) the name of a **method** of each Node in the tree, e.g. acme\$Get("levelZeroBased"), where e.g. acme\$levelZeroBased <- function() acme\$level 1
- c.) a **function**, whose first argument must be a Node e.g. acme\$Get(function(node) node\$cost * node\$p)

... in case the attribute is a function or a method, the ellipsis is passed to it as

additional arguments.

format if FALSE (the default), no formatting is being used. If TRUE, then the first for-

matter (if any) found along the ancestor path is being used for formatting (see SetFormat). If format is a function, then the collected value is passed to that

function, and the result is returned.

inheritFromAncestors

if TRUE, then the path above a Node is searched to get the attribute in case it

is NULL.

nullAsNa If TRUE (the default), then NULL is returned as NA. Otherwise it is returned as

NULL.

Examples

```
data(acme)
GetAttribute(acme$IT$Outsource, "cost")
```

GetPhyloNr

Determine the number a Node has after conversion to a phylo object

Description

Use this function when plotting a Node as a phylo, e.g. to set custom labels to plot.

isLeaf 35

Usage

```
GetPhyloNr(x, type = c("node", "edge"))
```

Arguments

x The Node

type Either "node" (the default) or "edge" (to get the number of the edge from x to its

parent)

Value

an integer representing the node

See Also

```
Other ape phylo conversions: as.Node.phylo(), as.phylo.Node()
```

Examples

```
library(ape)
library(data.tree)
data(acme)
ap <- as.phylo(acme)
#plot(ap)
#nodelabels("IT Dep.", GetPhyloNr(Climb(acme, "IT")))
#edgelabels("Good!", GetPhyloNr(Climb(acme, "IT", "Switch to R"), "edge"))</pre>
```

isLeaf

Check if a Node is a leaf

Description

Check if a Node is a leaf

Usage

```
isLeaf(node)
```

Arguments

node

The Node to test.

Value

TRUE if the Node is a leaf, FALSE otherwise

36 isNotRoot

isNotLeaf

Check if a Node is not a leaf

Description

Check if a Node is not a leaf

Usage

isNotLeaf(node)

Arguments

node

The Node to test.

Value

FALSE if the Node is a leaf, TRUE otherwise

isNotRoot

Check if a Node is not a root

Description

Check if a Node is not a root

Usage

isNotRoot(node)

Arguments

node

The Node to test.

Value

FALSE if the Node is the root, TRUE otherwise

isRoot 37

isRoot

Check if a Node is the root

Description

Check if a Node is the root

Usage

isRoot(node)

Arguments

node

The Node to test.

Value

TRUE if the Node is the root, FALSE otherwise

mushroom

Sample Data: Data Used by the ID3 Vignette

Description

mushroom contains attributes of mushrooms. We can use this data to predict a mushroom's toxicity based on its attributes. The attributes available in the data set are:

Usage

data(mushroom)

Format

data.frame

Details

- color the color of a mushroom
- size whether a mushroom is small or large
- points whether a mushroom has points
- edibility whether a mushroom is edible or toxic

Node Node

Navigate

Navigate to another node by relative path.

Description

Navigate to another node by relative path.

Usage

```
Navigate(node, path)
```

Arguments

node The starting Node to navigate

path A string or a character vector describing the path to navigate

Details

The path is always relative to the node. Navigation to the parent is defined by ..., whereas navigation to a child is defined via the child's name. If path is provided as a string, then the navigation steps are separated by '/'.

See Also

Climb

Examples

```
data(acme)
Navigate(acme$Research, "../IT/Outsource")
Navigate(acme$Research, c("..", "IT", "Outsource"))
```

Node

Create a data.tree Structure With Nodes

Description

Node is at the very heart of the data. tree package. All trees are constructed by tying together Node objects.

Usage

```
# n1 <- Node$new("Node 1")
```

Format

An R6Class generator object

Details

Assemble Node objects into a data. tree structure and use the traversal methods to set, get, and perform operations on it. Typically, you construct larger tree structures by converting from data. frame, list, or other formats.

Most methods (e.g. node\$Sort()) also have a functional form (e.g. Sort(node))

Active bindings

name Gets or sets the name of a Node. For example Node\$name <- "Acme".

printFormatters gets or sets the formatters used to print a Node. Set this as a list to a root node. The different formatters are h (horizontal), v (vertical), l (L), j (junction), and s (separator). For example, you can set the formatters to list(h = "\u2500", v = "\u2502", l = "\u2514", j = "\u251C", s = " ") to get a similar behavior as in fs::dir_tree(). The defaults are: list(h = "--", v = "\u00A6", l = "\u00B0", j = "\u00A6", s = " ")

parent Gets or sets the parent Node of a Node. Only set this if you know what you are doing, as you might mess up the tree structure!

children Gets or sets the children list of a Node. Only set this if you know what you are doing, as you might mess up the tree structure!

isLeaf Returns TRUE if the Node is a leaf, FALSE otherwise

isRoot Returns TRUE if the Node is the root, FALSE otherwise

count Returns the number of children of a Node

totalCount Returns the total number of Nodes in the tree

path Returns a vector of mode character containing the names of the Nodes in the path from the root to this Node

pathString Returns a string representing the path to this Node, separated by backslash

position The position of a Node within its siblings

fields Will be deprecated, use attributes instead

fieldsAll Will be deprecated, use attributesAll instead

attributes The attributes defined on this specific node

attributesAll The distinct union of attributes defined on all the nodes in the tree spanned by this Node

levelName Returns the name of the Node, preceded by level times '*'. Useful for printing and not typically called by package users.

leaves Returns a list containing all the leaf Nodes

leafCount Returns the number of leaves are below a Node

level Returns an integer representing the level of a Node. For example, the root has level 1.

height Returns max(level) of any of the Nodes of the tree

isBinary Returns TRUE if all Nodes in the tree (except the leaves) have count = 2

Node Node

```
root Returns the root of a Node in a tree.
siblings Returns a list containing all the siblings of this Node
averageBranchingFactor Returns the average number of crotches below this Node
```

Methods

Public methods:

- Node\$new()
- Node\$AddChild()
- Node\$AddChildNode()
- Node\$AddSibling()
- Node\$AddSiblingNode()
- Node\$RemoveChild()
- Node\$RemoveAttribute()
- Node\$Sort()
- Node\$Revert()
- Node\$Prune()
- Node\$Climb()
- Node\$Navigate()
- Node\$Get()
- Node\$Do()
- Node\$Set()
- Node\$clone()

Method new(): Create a new Node object. This is often used to create the root of a tree when creating a tree programmatically.

```
Usage:
Node$new(name, check = c("check", "no-warn", "no-check"), ...)
Arguments:
name the name of the node to be created
check Either
```

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors

... A name-value mapping of node attributes

```
Returns: A new 'Node' object
Examples:
node <- Node$new("mynode", x = 2, y = "value of y")
node$y</pre>
```

Method AddChild(): Creates a Node and adds it as the last sibling as a child to the Node on which this is called.

```
Usage:
Node$AddChild(name, check = c("check", "no-warn", "no-check"), ...)
Arguments:
name the name of the node to be created
check Either
```

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors
- ... A name-value mapping of node attributes

```
Returns: The new Node (invisibly)
Examples:
root <- Node$new("myroot", myname = "I'm the root")
root$AddChild("child1", myname = "I'm the favorite child")
child2 <- root$AddChild("child2", myname = "I'm just another child")
child3 <- child2$AddChild("child3", myname = "Grandson of a root!")
print(root, "myname")</pre>
```

Method AddChildNode(): Adds a Node as a child to this node.

```
Usage:
Node$AddChildNode(child)
Arguments:
child The child "Node" to add.
Returns: the child node added (this lets you chain calls)
Examples:
root <- Node$new("myroot")
child <- Node$new("mychild")
root$AddChildNode(child)</pre>
```

Method AddSibling(): Creates a new Node called name and adds it after this Node as a sibling.

```
Usage:
Node$AddSibling(name, check = c("check", "no-warn", "no-check"), ...)
Arguments:
name the name of the node to be created
check Either
```

• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)

- "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)
- "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors
- ... A name-value mapping of node attributes

```
Returns: the sibling node (this lets you chain calls)
```

```
Examples:
```

```
#' root <- Node$new("myroot")
child <- root$AddChild("child1")
sibling <- child$AddSibling("sibling1")</pre>
```

Method AddSiblingNode(): Adds a Node after this Node, as a sibling.

```
Usage:
```

```
Node$AddSiblingNode(sibling)
```

Arguments:

sibling The "Node" to add as a sibling.

Returns: the added sibling node (this lets you chain calls, as in the examples)

Examples:

```
root <- Node$new("myroot")
child <- Node$new("mychild")
sibling <- Node$new("sibling")
root$AddChildNode(child)$AddSiblingNode(sibling)</pre>
```

Method RemoveChild(): Remove the child Node called name from a Node and returns it.

Usage:

Node\$RemoveChild(name)

Arguments:

name the name of the node to be created

Returns: the subtree spanned by the removed child.

Examples:

```
node <- Node$new("myroot")$AddChild("mychild")$root
node$RemoveChild("mychild")</pre>
```

Method RemoveAttribute(): Removes attribute called name from this Node.

Usage:

```
Node$RemoveAttribute(name, stopIfNotAvailable = TRUE)
```

Arguments:

```
name the name of the node to be created
```

stopIfNotAvailable Gives an error if stopIfNotAvailable and the attribute does not exist.

Examples:

```
node <- Node$new("mynode")
node$RemoveAttribute("age", stopIfNotAvailable = FALSE)
node$age <- 27
node$RemoveAttribute("age")
node</pre>
```

Method Sort(): Sort children of a Node or an entire data. tree structure

Usage:

```
Node$Sort(attribute, ..., decreasing = FALSE, recursive = TRUE)
```

Arguments:

attribute determines what is collected. The attribute can be

- a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme\$Get("p") or acme\$Get("position")
- b.) the name of a **method** of each Node in the tree, e.g. acme\$Get("levelZeroBased"), where e.g. acme\$levelZeroBased <- function() acme\$level 1
- c.) a **function**, whose first argument must be a Node e.g. acme\$Get(function(node) node\$cost * node\$p)

... any parameters to be passed on the the attribute (in case it's a method or a function) decreasing sort order

recursive if TRUE, the method will be called recursively on the Node's children. This allows sorting an entire tree.

Details: You can sort with respect to any argument of the tree. But note that sorting has side-effects, meaning that you modify the underlying, original data.tree object structure. See also Sort for the equivalent function.

Returns: Returns the node on which Sort is called, invisibly. This can be useful to chain Node methods.

```
Examples:
```

```
data(acme)
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")
Sort(acme, "totalCost", decreasing = FALSE)
print(acme, "totalCost")</pre>
```

Method Revert(): Reverts the sort order of a Node's children.

See also Revert for the equivalent function.

Usage:

```
Node$Revert(recursive = TRUE)
```

Arguments:

recursive if TRUE, the method will be called recursively on the Node's children. This allows sorting an entire tree.

Node Node

Returns: returns the Node invisibly (for chaining)

```
Method Prune(): Prunes a tree.
```

Pruning refers to removing entire subtrees. This function has side-effects, it modifies your data.tree structure!

See also Prune for the equivalent function.

```
Usage:
```

Node\$Prune(pruneFun)

Arguments:

pruneFun allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.

Returns: the number of nodes removed

```
Examples:
```

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum))
Prune(acme, function(x) x$cost > 700000)
```

Method Climb(): Climb a tree from parent to children, by provided criteria.

```
Usage:
```

```
Node$Climb(...)
```

print(acme, "cost")

Arguments:

... an attribute-value pairlist to be searched. For brevity, you can also provide a character vector to search for names.

node The root Node of the tree or subtree to climb

Details: This method lets you climb the tree, from crutch to crutch. On each Node, the Climb finds the first child having attribute value equal to the provided argument.

```
See also Climb and Navigate
```

Climb(node, ...)

Returns: the Node having path . . . , or NULL if such a path does not exist

Examples:

data(acme)

```
#the following are all equivalent
Climb(acme, 'IT', 'Outsource')
Climb(acme, name = 'IT', name = 'Outsource')
Climb(acme, 'IT')$Climb('Outsource')
Navigate(acme, path = "IT/Outsource")
Climb(acme, name = 'IT')
Climb(acme, position = c(2, 1))
```

```
#or, equivalent:
 Climb(acme, position = 2, position = 1)
 Climb(acme, name = "IT", cost = 250000)
 tree <- CreateRegularTree(5, 2)</pre>
 tree Climb(c("1", "1"), position = c(2, 2))path
Method Navigate(): Navigate to another node by relative path.
 Usage:
 Node$Navigate(path)
 Arguments:
 path A string or a character vector describing the path to navigate
 node The starting Node to navigate
 Details: The path is always relative to the Node. Navigation to the parent is defined by ...
 whereas navigation to a child is defined via the child's name. If path is provided as a string, then
 the navigation steps are separated by '/'.
 See also Navigate and Climb
 Examples:
 data(acme)
 Navigate(acme$Research, "../IT/Outsource")
 Navigate(acme$Research, c("..", "IT", "Outsource"))
Method Get(): Traverse a Tree and Collect Values
 Usage:
 Node$Get(
   attribute,
    traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
   pruneFun = NULL,
   filterFun = NULL,
   format = FALSE,
    inheritFromAncestors = FALSE,
    simplify = c(TRUE, FALSE, "array", "regular")
 )
 Arguments:
 attribute determines what is collected. The attribute can be
     • a.) the name of a field or a property/active of each Node in the tree, e.g. acme$Get("p")
       or acme$Get("position")
     • b.) the name of a method of each Node in the tree, e.g. acme$Get("levelZeroBased"),
       where e.g. acme$levelZeroBased <- function() acme$level - 1
```

• c.) a function, whose first argument must be a Node e.g. acme\$Get(function(node)

node\$cost * node\$p)

... in case the attribute is a function or a method, the ellipsis is passed to it as additional arguments.

traversal defines the traversal order to be used. This can be

pre-order Go to first child, then to its first child, etc.

post-order Go to the first branch's leaf, then to its siblings, and work your way back to the root

in-order Go to the first branch's leaf, then to its parent, and only then to the leaf's sibling **level** Collect root, then level 2, then level 3, etc.

ancestor Take a node, then the node's parent, then that node's parent in turn, etc. This ignores the pruneFun

function You can also provide a function, whose sole parameter is a Node object. The function is expected to return the node's next node, a list of the node's next nodes, or NULL.

Read the data.tree vignette for a detailed explanation of these traversal orders.

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.

filterFun allows providing a a filter, i.e. a function taking a Node as an input, and returning TRUE or FALSE. Note that if filter returns FALSE, then the node will be excluded from the result (but not the entire subtree).

format if FALSE (the default), no formatting is being used. If TRUE, then the first formatter (if any) found along the ancestor path is being used for formatting (see SetFormat). If format is a function, then the collected value is passed to that function, and the result is returned.

inheritFromAncestors if TRUE, then the path above a Node is searched to get the attribute in case it is NULL.

simplify same as sapply, i.e. TRUE, FALSE or "array". Additionally, you can specify "regular" if each returned value is of length > 1, and equally named. See below for an example.

Details: The Get method is one of the most important ones of the data.tree package. It lets you traverse a tree and collect values along the way. Alternatively, you can call a method or a function on each Node.

See also Get, Node, Set, Do, Traverse

Returns: a vector containing the atrributes collected during traversal, in traversal order. NULL is converted to NA, such that length(Node\$Get) == Node\$totalCount

```
#simplify = "regular" will preserve names
 acme$Get(function(x) c(position = x$position, level = x$level), simplify = "regular")
Method Do(): Executes a function on a set of nodes
 Usage:
 Node$Do(
    fun,
    traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
    pruneFun = NULL,
    filterFun = NULL
 )
 Arguments:
 fun the function to execute. The function is expected to be either a Method, or to take a Node
     as its first argument
 ... A name-value mapping of node attributes
 traversal defines the traversal order to be used. This can be
     pre-order Go to first child, then to its first child, etc.
     post-order Go to the first branch's leaf, then to its siblings, and work your way back to the
        root
     in-order Go to the first branch's leaf, then to its parent, and only then to the leaf's sibling
     level Collect root, then level 2, then level 3, etc.
     ancestor Take a node, then the node's parent, then that node's parent in turn, etc. This
        ignores the pruneFun
     function You can also provide a function, whose sole parameter is a Node object. The
        function is expected to return the node's next node, a list of the node's next nodes, or
     Read the data.tree vignette for a detailed explanation of these traversal orders.
 pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and
     returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its
     entire sub-tree will not be considered.
 filterFun allows providing a a filter, i.e. a function taking a Node as an input, and returning
     TRUE or FALSE. Note that if filter returns FALSE, then the node will be excluded from the
     result (but not the entire subtree).
 Details: See also Node, Get, Set, Traverse
 Examples:
 data(acme)
 acme$Do(function(node) node$expectedCost <- node$p * node$cost)</pre>
 print(acme, "expectedCost")
```

Method Set(): Traverse a Tree and Assign Values

```
Usage:
Node$Set(
  . . . ,
  traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
  pruneFun = NULL,
  filterFun = NULL
)
Arguments:
... each argument can be a vector of values to be assigned. Recycled.
traversal defines the traversal order to be used. This can be
    pre-order Go to first child, then to its first child, etc.
    post-order Go to the first branch's leaf, then to its siblings, and work your way back to the
    in-order Go to the first branch's leaf, then to its parent, and only then to the leaf's sibling
    level Collect root, then level 2, then level 3, etc.
    ancestor Take a node, then the node's parent, then that node's parent in turn, etc. This
      ignores the pruneFun
    function You can also provide a function, whose sole parameter is a Node object. The
      function is expected to return the node's next node, a list of the node's next nodes, or
      NULL.
    Read the data.tree vignette for a detailed explanation of these traversal orders.
pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and
    returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its
    entire sub-tree will not be considered.
filterFun allows providing a a filter, i.e. a function taking a Node as an input, and returning
    TRUE or FALSE. Note that if filter returns FALSE, then the node will be excluded from the
    result (but not the entire subtree).
Details: The method takes one or more vectors as an argument. It traverses the tree, whereby
the values are picked from the vector. Also available as OO-style method on Node.
See also Node, Get, Do, Traverse
Returns: invisibly returns the nodes (useful for chaining)
Examples:
data(acme)
acme$Set(departmentId = 1:acme$totalCount, openingHours = NULL, traversal = "post-order")
acme$Set(head = c("Jack Brown",
                     "Mona Moneyhead",
                     "Dr. Frank N. Stein",
                      "Eric Nerdahl"
                     ),
           filterFun = function(x) !x$isLeaf
```

Method clone(): The objects of this class are cloneable with this method.

print(acme, "departmentId", "head")

```
Usage:
Node$clone(deep = FALSE)
Arguments:
deep Whether to make a deep clone.
```

See Also

For more details see the data.tree documentations, or the data.tree vignette: vignette("data.tree")
Node
Sort

```
library(data.tree)
acme <- Node$new("Acme Inc.")</pre>
accounting <- acme$AddChild("Accounting")$</pre>
            AddSibling("Research")$
            AddChild("New Labs")$
            parent$
            AddSibling("IT")$
            AddChild("Outsource")
print(acme)
## -----
## Method `Node$new`
## -----
node <- Nodenew("mynode", x = 2, y = "value of y")
node$y
## Method `Node$AddChild`
root <- Node$new("myroot", myname = "I'm the root")</pre>
root$AddChild("child1", myname = "I'm the favorite child")
child2 <- root$AddChild("child2", myname = "I'm just another child")</pre>
child3 <- child2$AddChild("child3", myname = "Grandson of a root!")</pre>
print(root, "myname")
## Method `Node$AddChildNode`
## -----
root <- Node$new("myroot")</pre>
child <- Node$new("mychild")</pre>
root$AddChildNode(child)
```

Node Node

```
## Method `Node$AddSibling`
## -----
#' root <- Node$new("myroot")</pre>
child <- root$AddChild("child1")</pre>
sibling <- child$AddSibling("sibling1")</pre>
## -----
## Method `Node$AddSiblingNode`
## -----
root <- Node$new("myroot")</pre>
child <- Node$new("mychild")</pre>
sibling <- Node$new("sibling")</pre>
root$AddChildNode(child)$AddSiblingNode(sibling)
## -----
## Method `Node$RemoveChild`
node <- Node$new("myroot")$AddChild("mychild")$root</pre>
node$RemoveChild("mychild")
## -----
## Method `Node$RemoveAttribute`
## -----
node <- Node$new("mynode")</pre>
node$RemoveAttribute("age", stopIfNotAvailable = FALSE)
node$age <- 27
node$RemoveAttribute("age")
node
## Method `Node$Sort`
## -----
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")</pre>
Sort(acme, "totalCost", decreasing = FALSE)
print(acme, "totalCost")
## -----
## Method `Node$Prune`
## -----
```

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum))</pre>
Prune(acme, function(x) x$cost > 700000)
print(acme, "cost")
## Method `Node$Climb`
data(acme)
#the following are all equivalent
Climb(acme, 'IT', 'Outsource')
Climb(acme, name = 'IT', name = 'Outsource')
Climb(acme, 'IT')$Climb('Outsource')
Navigate(acme, path = "IT/Outsource")
Climb(acme, name = 'IT')
Climb(acme, position = c(2, 1))
#or, equivalent:
Climb(acme, position = 2, position = 1)
Climb(acme, name = "IT", cost = 250000)
tree <- CreateRegularTree(5, 2)</pre>
tree Climb(c("1", "1"), position = c(2, 2))path
## -----
## Method `Node$Navigate`
## -----
data(acme)
Navigate(acme$Research, "../IT/Outsource")
Navigate(acme$Research, c("..", "IT", "Outsource"))
## Method `Node$Get`
data(acme)
acme$Get("level")
acme$Get("totalCount")
acme$Get(function(node) node$cost * node$p,
        filterFun = isLeaf)
#This is equivalent:
```

```
nodes <- Traverse(acme, filterFun = isLeaf)</pre>
Get(nodes, function(node) node$cost * node$p)
#simplify = "regular" will preserve names
acme\$Get(function(x) c(position = x\$position, level = x\$level), simplify = "regular")
## -----
## Method `Node$Do`
data(acme)
acme$Do(function(node) node$expectedCost <- node$p * node$cost)</pre>
print(acme, "expectedCost")
## -----
## Method `Node$Set`
## -----
data(acme)
acme\$Set(departmentId = 1:acme\$totalCount, \ openingHours = NULL, \ traversal = "post-order")
acme$Set(head = c("Jack Brown",
               "Mona Moneyhead",
               "Dr. Frank N. Stein",
               "Eric Nerdahl"
               ),
       filterFun = function(x) !x$isLeaf
print(acme, "departmentId", "head")
```

NODE_RESERVED_NAMES_CONST

Names that are reserved by the Node class.

Description

These are reserved by the Node class, you cannot use these as attribute names. Note also that all attributes starting with a . are reserved.

Usage

```
NODE_RESERVED_NAMES_CONST
```

Format

An object of class character of length 43.

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plot.Node

Plot a graph, or get a graphviz dot representation of the tree

Description

Use these methods to style your graph, and to plot it. The functionality is built around the DiagrammeR package, so for anything that goes beyond simple plotting, it is recommended to read its documentation at https://rich-iannone.github.io/DiagrammeR/docs.html. Note that DiagrammeR is only suggested by data.tree, so 'plot' only works if you have installed it on your system.

Usage

```
## S3 method for class 'Node'
plot(
    x,
    ...,
    direction = c("climb", "descend"),
    pruneFun = NULL,
    output = "graph"
)

ToDiagrammeRGraph(root, direction = c("climb", "descend"), pruneFun = NULL)

SetNodeStyle(node, inherit = TRUE, keepExisting = FALSE, ...)

SetEdgeStyle(node, inherit = TRUE, keepExisting = FALSE, ...)

SetGraphStyle(root, keepExisting = FALSE, ...)

GetDefaultTooltip(node)
```

Arguments

X	The root node of the data.tree structure to plot
• • •	For the SetStyle methods, this can be any stlyeName / value pair. See https://graphviz.org/Documentation. for details. For the plot.Node generic method, this is not used.
direction	when converting to a network, should the edges point from root to children ("climb") or from child to parent ("descend")?
pruneFun	allows providing a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
output	A string specifying the output type; graph (the default) renders the graph using the grViz() function and visNetwork renders the graph using the visnetwork() function.
root	The root Node of the data tree structure to visualize.

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node The Node of the data.tree structure on which you would like to set style at-

tributes.

inherit If TRUE, then children will inherit this node's style. Otherwise they inherit from

this node's parent. Note that the inherit always applies to the node, i.e. all style

attributes of a node and not to a single style attribute.

keepExisting If TRUE, then style attributes are added to possibly existing style attributes on

the node.

Details

Use SetNodeStyle and SetEdgeStyle to define the style of your plot. Use plot to display a graphical representation of your tree.

The most common styles that can be set on the nodes are:

- color
- fillcolor
- fixedsize true or false
- fontcolor
- fontname
- fontsize
- height
- penwidth
- shape box, ellipse, polygon, circle, box, etc.
- style
- tooltip
- width

The most common styles that can be set on the edges are:

- arrowhead e.g. normal, dot, vee
- arrowsize
- arrowtail
- color
- dir forward, back, both, none
- fontcolor
- fontname
- fontsize
- headport
- label
- minlen
- penwidth
- tailport

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• tooltip

A good source to understand the attributes is https://graphviz.org/Documentation.php. Another good source is the DiagrammeR package documentation, or more specifically: https://rich-iannone.github.io/DiagrammeR/documentation.

In addition to the standard GraphViz functionality, the data.tree plotting infrastructure takes advantage of the fact that data.tree structure are always hierarchic. Thus, style attributes are inherited from parents to children on an individual basis. For example, you can set the fontcolor to red on a parent, and then all children will also have red font, except if you specifically disallow inheritance. Labels and tooltips are never inherited.

Another feature concerns functions: Instead of setting a fixed value (e.g. SetNodeStyle(acme, label = "Acme. Inc"), you can set a function (e.g. SetNodeStyle(acme, label = function(x) x\$name)). The function must take a Node as its single argument. Together with inheritance, this becomes a very powerful tool.

The GetDefaultTooltip method is a utility method that can be used to print all attributes of a Node.

There are some more examples in the 'applications' vignette, see vignette('applications', package = "data.tree")

```
data(acme)
SetGraphStyle(acme, rankdir = "TB")
SetEdgeStyle(acme, arrowhead = "vee", color = "blue", penwidth = 2)
#per default, Node style attributes will be inherited:
SetNodeStyle(acme, style = "filled,rounded", shape = "box", fillcolor = "GreenYellow",
             fontname = "helvetica", tooltip = GetDefaultTooltip)
SetNodeStyle(acme$IT, fillcolor = "LightBlue", penwidth = "5px")
#inheritance can be avoided:
SetNodeStyle(acme$Accounting, inherit = FALSE, fillcolor = "Thistle",
             fontcolor = "Firebrick", tooltip = "This is the accounting department")
SetEdgeStyle(acme$Research$`New Labs`,
             color = "red",
             label = "Focus!",
             penwidth = 3,
             fontcolor = "red")
#use Do to set style on specific nodes:
Do(acme$leaves, function(node) SetNodeStyle(node, shape = "egg"))
plot(acme)
#print p as label, where available:
SetNodeStyle(acme, label = function(node) node$p)
plot(acme)
```

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Description

Print a Node in a human-readable fashion.

Usage

```
## S3 method for class 'Node'
print(
    x,
    ...,
    pruneMethod = c("simple", "dist", NULL),
    limit = 100,
    pruneFun = NULL,
    row.names = T
)
```

Arguments

x The Node

... Node attributes to be printed. Can be either a character (i.e. the name of a Node

field), a Node method, or a function taking a Node as a single argument. See

Get for details on the meaning of attribute.

pruneMethod The method can be used to prune for printing in a simple way. If NULL, the

entire tree is displayed. If "simple", then only the first limit nodes are displayed. If "dist", then Nodes are removed everywhere in the tree, according to

their level. If pruneFun is provided, then pruneMethod is ignored.

limit The maximum number of nodes to print. Can be NULL if the entire tree should

be printed.

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and

returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the

Node and its entire sub-tree will not be considered.

row.names If TRUE (default), then the row names are printed out. Else, they are not.

```
data(acme)
print(acme, "cost", "p")
print(acme, "cost", probability = "p")
print(acme, expectedCost = function(x) x$cost * x$p)
do.call(print, c(acme, acme$attributesAll))

tree <- CreateRegularTree(4, 5)
# print entire tree:
print(tree, pruneMethod = NULL)
# print first 20 nodes:
print(tree, pruneMethod = "simple", limit = 20)
# print 20 nodes, removing leafs first:
print(tree, pruneMethod = "dist", limit = 20)
# provide your own pruning function:</pre>
```

Prune 57

```
print(tree, pruneFun = function(node) node$position != 2)
```

Prune

Prunes a tree.

Description

Pruning refers to removing entire subtrees. This function has side-effects, it modifies your data.tree structure!

Usage

```
Prune(node, pruneFun)
```

Arguments

node The root of the sub-tree to be pruned

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and

returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the

Node and its entire sub-tree will not be considered.

Value

the number of nodes removed

See Also

Node

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum))
Prune(acme, function(x) x$cost > 700000)
print(acme, "cost")
```

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Revert

Reverts the sort order of a Node's children.

Description

Reverts the sort order of a Node's children.

Usage

```
Revert(node, recursive = TRUE)
```

Arguments

node the Node whose childrens' sort order is to be reverted recursive If TRUE, then revert is called recursively on all children.

Value

returns the Node invisibly (for chaining)

See Also

Node

Sort

Set

Traverse a Tree and Assign Values

Description

The method takes one or more vectors as an argument. It traverses the tree, whereby the values are picked from the vector. Also available as OO-style method on Node.

Usage

```
#00-style:
# node$Set(...,
# traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
# pruneFun = NULL,
# filterFun = NULL)
#traditional:
Set(nodes, ...)
```

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Arguments

nodes The nodes on which to perform the Get (typically obtained via Traverse)
... each argument can be a vector of values to be assigned. Recycled.

Value

invisibly returns the nodes (useful for chaining)

See Also

Node

Get

Do

Traverse

Examples

SetFormat

Set a formatter function on a specific node

Description

Formatter functions set on a Node act as a default formatter when printing and using the Get method. The formatter is inherited, meaning that whenever Get fetches an attribute from a Node, it checks on the Node or on any of its ancestors whether a formatter is set.

Usage

```
SetFormat(node, name, formatFun)
```

Arguments

node The node on which to set the formatter

name The attribute name for which to set the formatter

formatFun The formatter, i.e. a function taking a value as an input, and formatting returning

the formatted value

60 Sort

See Also

Get print.Node

Examples

```
data(acme)
acme$Set(id = 1:(acme$totalCount))
SetFormat(acme, "id", function(x) FormatPercent(x, digits = 0))
SetFormat(Climb(acme, "IT"), "id", FormatFixedDecimal)
print(acme, "id")
# Calling Get with an explicit formatter will overwrite the default set on the Node:
print(acme, id = acme$Get("id", format = function(x) paste0("id:", x)))
# Or, to avoid formatters, even though you set them on a Node:
print(acme, id = acme$Get("id", format = identity))
```

Sort

Sort children of a Node or an entire data. tree structure

Description

You can sort with respect to any argument of the tree. But note that sorting has side-effects, meaning that you modify the underlying, original data.tree object structure.

Usage

```
Sort(node, attribute, ..., decreasing = FALSE, recursive = TRUE)
```

Arguments

The node whose children are to be sorted node determines what is collected. The attribute can be attribute • a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme\$Get("p") or acme\$Get("position") • b.) the name of a **method** of each Node in the tree, e.g. acme\$Get("levelZeroBased"), where e.g. acme\$levelZeroBased <- function() acme\$level - 1 • c.) a **function**, whose first argument must be a Node e.g. acme\$Get(function(node) node\$cost * node\$p) any parameters to be passed on the the attribute (in case it's a method or a function) decreasing recursive if TRUE, Sort will be called recursively on the Node's children. This allows sorting an entire tree.

ToNewick 61

Value

Returns the node on which Sort is called, invisibly. This can be useful to chain Node methods.

See Also

Node

Revert

Examples

```
data(acme)
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")
Sort(acme, "totalCost", decreasing = FALSE)
print(acme, "totalCost")</pre>
```

ToNewick

Write a data. tree structure to Newick notation

Description

To read from Newick, you can use the ape package, and convert the resulting phylo object to a data.tree structure.

Usage

```
ToNewick(node, heightAttribute = DefaultPlotHeight, ...)
```

Arguments

node $$\operatorname{\textbf{The}}$ root Node of a tree or sub-tree to be converted height Attribute

The attribute (field name, method, or function) storing or calculating the height

for each Node

... parameters that will be passed on the heightAttributeName, in case it is a function

See Also

Other Conversions from Node: as.dendrogram.Node()

```
data(acme)
ToNewick(acme)
ToNewick(acme, heightAttribute = NULL)
ToNewick(acme, heightAttribute = function(x) DefaultPlotHeight(x, 200))
ToNewick(acme, rootHeight = 200)
```

62 Traverse

Traverse	Traverse a tree or a sub-tree

Description

Traverse takes the root of a tree or a sub-tree, and "walks" the tree in a specific order. It returns a list of Node objects, filtered and pruned by filterFun and pruneFun.

Usage

```
Traverse(
  node,
  traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
  pruneFun = NULL,
  filterFun = NULL
)
```

Arguments

node the root of a tree or a sub-tree that should be traversed

any of 'pre-order' (the default), 'post-order', 'in-order', 'level', 'ancestor', or a

custom function (see details)

pruneFun allows providing a prune criteria, i.e. a function taking a Node as an input, and

returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the

Node and its entire sub-tree will not be considered.

filterFun allows providing a a filter, i.e. a function taking a Node as an input, and returning

TRUE or FALSE. Note that if filter returns FALSE, then the node will be excluded

from the result (but not the entire subtree).

Details

The traversal order is as follows. (Note that these descriptions are not precise and complete. They are meant for quick reference only. See the data.tree vignette for a more detailed description).

pre-order Go to first child, then to its first child, etc.

post-order Go to the first branch's leaf, then to its siblings, and work your way back to the root **in-order** Go to the first branch's leaf, then to its parent, and only then to the leaf's sibling **level** Collect root, then level 2, then level 3, etc.

ancestor Take a node, then the node's parent, then that node's parent in turn, etc. This ignores the pruneFun

function You can also provide a function, whose sole parameter is a Node object. The function is expected to return the node's next node, a list of the node's next nodes, or NULL.

Value

a list of Nodes

Traverse 63

See Also

Node

Get

Set

Do

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